

FIGURE 1

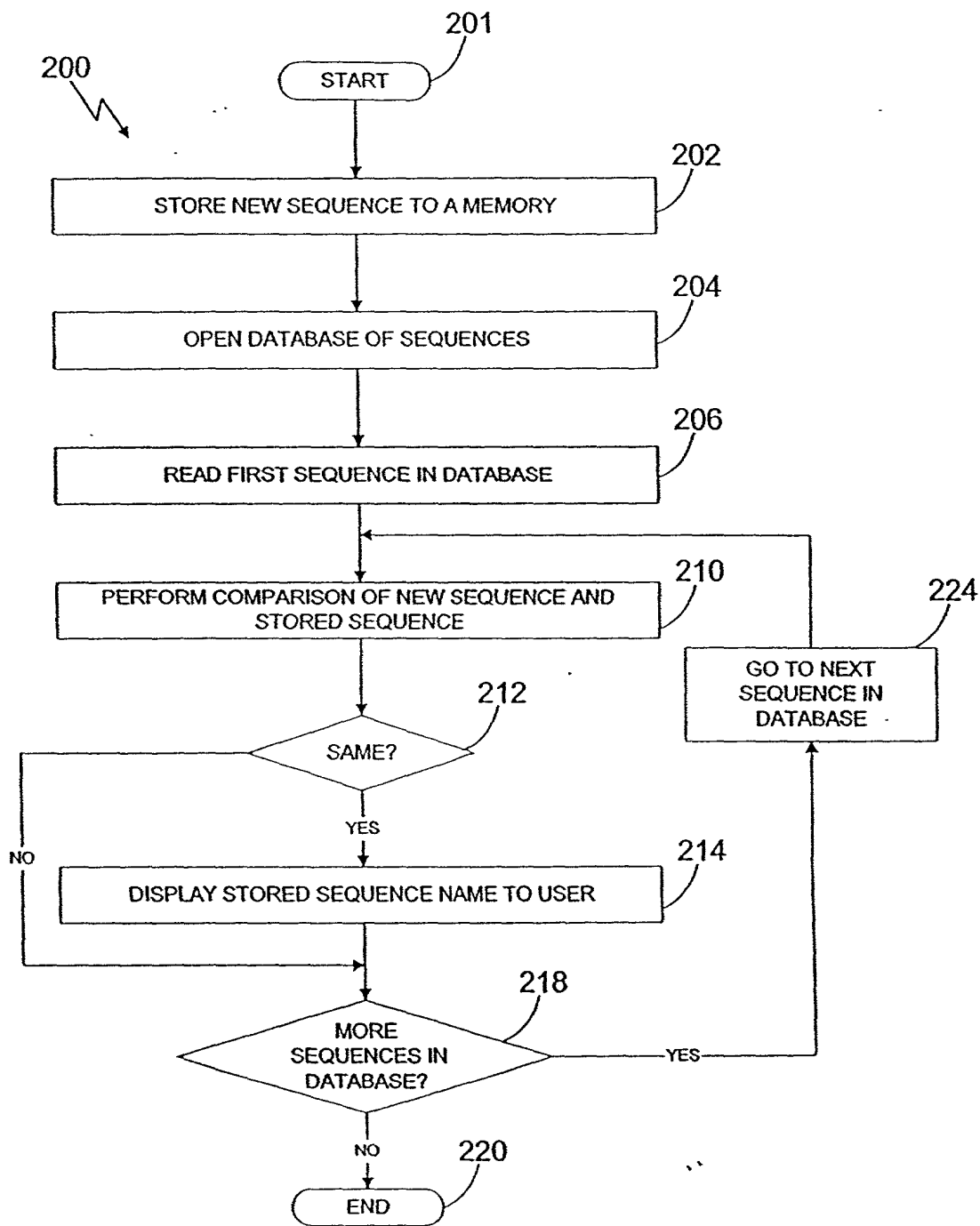


FIGURE 2

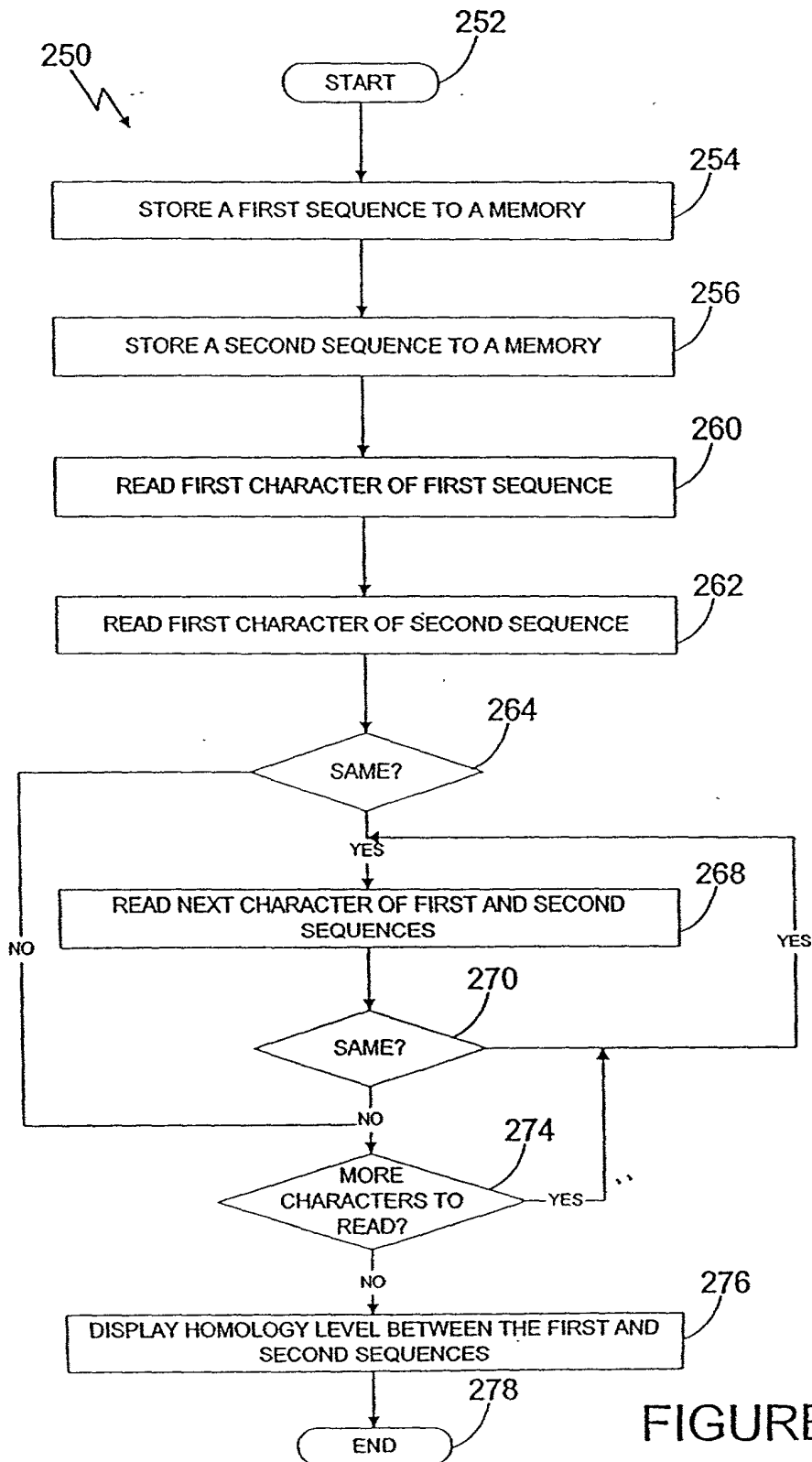


FIGURE 3

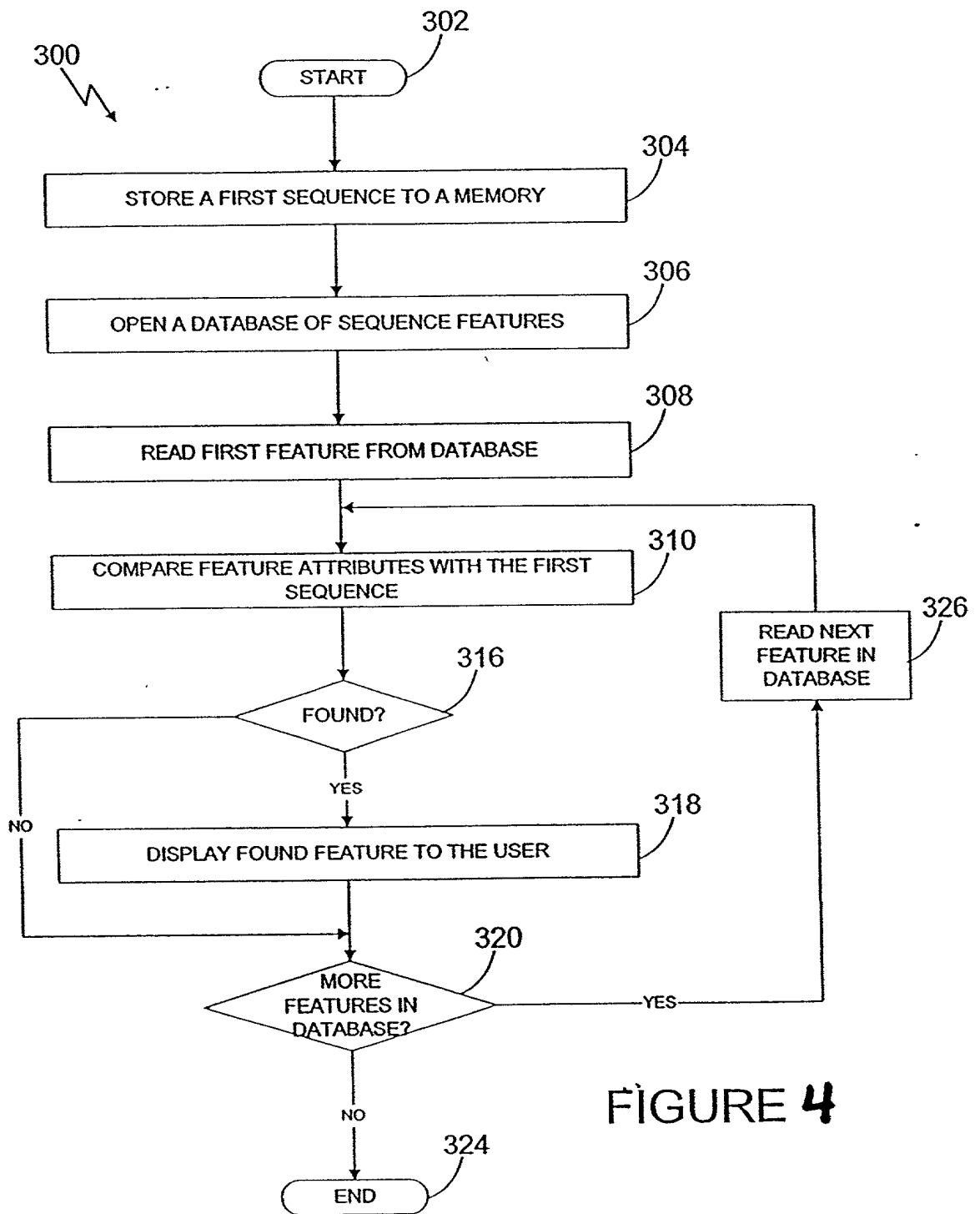


FIGURE 4

# FIGURE 5

*Ammonifex degensii* KC4 Phosphatase(3A1A=3A2A)

Complete gene sequence

1 ATGAGGGGGAGCGGAGTGC GGATACTTCTCACCAACGATGACGGCATCTTTGCCGAGGGT  
 MetArgGlySerGlyValArgIleLeuLeuThrAsnAspAspGlyIlePheAlaGluGly  
 21 CTGGGGGCTCTGCGCAAGATGCTGGAGCCCGTGGCTACCCCTTTACGTGGTGGCTCCGGAC  
 LeuGlyAlaLeuArgLysMetLeuGluProValAlaThrLeuTyrValValAlaProAsp  
 41 CGAGAGCGTAGCGCGGCCAGCCATGCTATCACCGTTACCGCCCCCTGCGGGTGCGGGAG  
 ArgGluArgSerAlaAlaSerHisAlaIleThrValHisArgProLeuArgValArgGlu  
 61 GCGGGTTTTCGAGCCCCAGGCTTAAAGGCTGGGTAGTGGACGGTACCCCGCCGACTGC  
 AlaGlyPheArgSerProArgLeuLysGlyTrpValValAspGlyThrProAlaAspCys  
 81 GTCAAGCTGGGCCTGGAGGTACTTTTGGCCGAACGTCCAGATTTCTGGTTTCGGGCATA  
 ValLysLeuGlyLeuGluValLeuLeuProGluArgProAspPheLeuValSerGlyIle  
 101 AACTACGGGCCCCAACCTGGGTACCGACGTACTTTACTCCGGCACCGTCTCGGCGGCCATA  
 AsnTyrGlyProAsnLeuGlyThrAspValLeuTyrSerGlyThrValSerAlaAlaIle  
 121 GAAGGGGTAATTAACGGCATTCCTCGGTGGCCGTATCTTTGGCCACGCGCGGGAGCCG  
 GluGlyValIleAsnGlyIleProSerValAlaValSerLeuAlaThrArgArgGluPro  
 141 GACTATACCTGGGCGGCCCCGGTTCGTCTCTGGTCTGCTGGAGGAACTGCGAAAAACACCAA  
 AspTyrThrTrpAlaAlaArgPheValLeuValLeuLeuGluGluLeuArgLysHisGln  
 161 CTGCCCCCAGGAACCTGCTCAACGTCAACGTGCCCCGACGGGGTGCCCCGCGGGTCAAG  
 LeuProProGlyThrLeuLeuAsnValAsnValProAspGlyValProArgGlyValLys  
 181 GTGACCAAACCTGGGAAGCGTACGCTACGTCAACGTGGTAGACTGCCGCACCGACCCCTCGG  
 ValThrLysLeuGlySerValArgTyrValAsnValValAspCysArgThrAspProArg  
 201 GGGAAGGCTTACTACTGGATGGCGGGAGAACCATTTGGAGCTGGACGGCAACGACTCCGAA  
 GlyLysAlaTyrTyrTrpMetAlaGlyGluProLeuGluLeuAspGlyAsnAspSerGlu  
 221 ACCGACGTCTGGGCGGTGCGAGAAGGCTATATTTCCGTAACACCGGTCCAGATCGACCTT  
 ThrAspValTrpAlaValArgGluGlyTyrIleSerValThrProValGlnIleAspLeu  
 241 ACTAACTACGGCTTCTGGAAGAACTCAAAAAATGGCGTTTCAAGGATATCTTTTCTTCT  
 ThrAsnTyrGlyPheLeuGluGluLeuLysLysTrpArgPheLysAspIlePheSerSer  
 TAA  
 261 End 261

# FIGURE 6

## *Methanococcus igneus* K015 Phosphatase (9A1A) Complete Gene Sequence

ATGTTGGATATACTGCTTGTAAATGATGATGGCATTATTTCAAATGGATTAAATAGCTTTG  
 1 MetLeuAspIleLeuLeuValAsnAspAspGlyIleTyrSerAsnGlyLeuIleAlaLeu  
 AAGGATGCATTATTGGAAAAATTTAATGCGAGGATTACTATTGTAGCCCCAACAAATCAG  
 21 LysAspAlaLeuLeuGluLysPheAsnAlaArgIleThrIleValAlaProThrAsnGln  
 CAGAGTGGTATTGGTAGGGCAATAAGTTTATTCGAGCCGTTAAGGATAACTAAAACCAAA  
 41 GlnSerGlyIleGlyArgAlaIleSerLeuPheGluProLeuArgIleThrLysThrLys  
 TTAGCAGATGGTTCTTGGGGATATGCAGTTTCAGGAACCCCAACAGATTGCGTTATATTG  
 61 LeuAlaAspGlySerTrpGlyTyrAlaValSerGlyThrProThrAspCysValIleLeu  
 GGCATTTATGAGATATTAAAGAAGGTACCTGATGTAGTTATATCAGGAATAAACATTGGA  
 81 GlyIleTyrGluIleLeuLysLysValProAspValValIleSerGlyIleAsnIleGly  
 GAAAACCTTGGGACTGAAATAACAACCTTCTGGAACGTTGGGGGCTGCGTTTGAAGGGGCC  
 101 GluAsnLeuGlyThrGluIleThrThrSerGlyThrLeuGlyAlaAlaPheGluGlyAla  
 CATCATGGGGCTAAGGCATTAGCATCATCACTCCAAGTTACCTCTGACCATCTAAAGTTT  
 121 HisHisGlyAlaLysAlaLeuAlaSerSerLeuGlnValThrSerAspHisLeuLysPhe  
 AAAGAGGGGGAGACCCCAATAGACTTCACAGTCCCAGCAAGAATTACTGCAAATGTTGTT  
 141 LysGluGlyGluThrProIleAspPheThrValProAlaArgIleThrAlaAsnValVal  
 GAGAAGATGTTGGATTATGATTTCCCATGTGATGTCGTCAACTTAAACATTCCAGAAGGA  
 161 GluLysMetLeuAspTyrAspPheProCysAspValValAsnLeuAsnIleProGluGly  
 GCAACAGAAAAGACACCGATTGAAATCACAAGGTTGGCAAGGAAAATGTATACAACACAC  
 181 AlaThrGluLysThrProIleGluIleThrArgLeuAlaArgLysMetTyrThrThrHis  
 GTTGAGGAAAGAATAGATCCAAGAGGGAGGAGTTATTATTGGATTGATGGGTATCCTATT  
 201 ValGluGluArgIleAspProArgGlyArgSerTyrTyrTrpIleAspGlyTyrProIle  
 TTAGAGGAAGAGGAAGACACTGATGTCTATGTTGTTAGAAGAAAGGGACATATTTCTCTA  
 221 LeuGluGluGluGluAspThrAspValTyrValValArgArgLysGlyHisIleSerLeu  
 ACCCCATTAAACATTAGACACAACAATTAATAATTTAGAGGAATTTAAGAAAAAATATGAG  
 241 ThrProLeuThrLeuAspThrThrIleLysAsnLeuGluGluPheLysLysLysTyrGlu  
 AGAATATTAAATGAATGA  
 261 ArgIleLeuAsnGluEnd 266

[illegible]

ATGATGATGGAAATTCCTACCTCGCGAGGGAATAAAAGCTGCTGTAGAGGCACCTTCAAGGGTTA  
1 MetMetMetGluPheThrArgGluGlyIleLysAlaAlaValGluAlaLeuGlnGlyLeu  
GGAGAGATCTACGTAGTTGCCCAATGTTTCAAAGGAGCGCAAGTGAAGGGCAATGACC  
21 GlyGluIleTyrValValAlaProMetPheGlnArgSerAlaSerGlyArgAlaMetThr  
ATCCACAGACCTCTAAGGGCTAAAAGAATAAGTATGAACGGTGCAAAGCAGCCTATGCT  
41 IleHisArgProLeuArgAlaLysArgIleSerMetAsnGlyAlaLysAlaAlaTyrAla  
TTGGATGGAATGCCCGTTGATTGCGTTATCTTTGCCATGGCCAGATTGAGATTTCGAC  
61 LeuAspGlyMetProValAspCysValIlePheAlaMetAlaArgPheGlyAspPheAsp  
CTTGCAATAAGTGGTGTAACCTGGGAGAAAACATGAGCACCGAGATAACGGTTTCCGGG  
81 LeuAlaIleSerGlyValAsnLeuGlyGluAsnMetSerThrGluIleThrValSerGly  
ACTGCAAGCGCTGCAATAGAGGCTGCAACCCAAGAGATCCCAAGCATTCCCATAGCCCTG  
101 ThrAlaSerAlaAlaIleGluAlaAlaThrGlnGluIleProSerIleProIleSerLeu  
GAAGTTAATAGAGAAAAACACAAATTTGGTGAGGGCGAAGAGATTGACTTCTCAGCTGCC  
121 GluValAsnArgGluLysHisLysPheGlyGluGlyGluGluIleAspPheSerAlaAla  
AAGTATTTCTAAGAAAAATCGCAACGGCGGTTTTAAAGAGAGGCCCTCCCCAAAGGAGTC  
141 LysTyrPheLeuArgLysIleAlaThrAlaValLeuLysArgGlyLeuProLysGlyVal  
GATATGCTGAACGTCAACGTCCCTTATGATGCAAATGAAAGGACAGAGATAGCTTTTACT  
161 AspMetLeuAsnValAsnValProTyrAspAlaAsnGluArgThrGluIleAlaPheThr  
CGCCTGGCAAGAAGGATGTATAGGCCCTTCTATTGAAGAGCGCATAGACCCAAAGGGGAAT  
181 ArgLeuAlaArgArgMetTyrArgProSerIleGluGluArgIleAspProLysGlyAsn  
CCCTACTACTGGATAGTTGGAACCTCAGTGCCCTAAGGAGGCATTAGAGCCGGGAACGGAT  
201 ProTyrTyrTrpIleValGlyThrGlnCysProLysGluAlaLeuGluProGlyThrAsp  
ATGTATGTAGTTAAAGTTGAGAGAAAAGTTAGCGTGACTCCAATAAACATTGATATGACA  
221 MetTyrValValLysValGluArgLysValSerValThrProIleAsnIleAspMetThr  
GCAAGAGTGAATTTAGACGAGATTAAAAAGACTTTTAGAACTGTAG  
241 AlaArgValAsnLeuAspGluIleLysArgLeuLeuGluLeuEnd 255

# FIGURE 8

## *Thermococcus celer* Phosphatase (25A1A) Complete Gene Sequence

ATGAGAACCCTGACAATAAACACTGACGCGGAGGGGTTTCGTTTTGAGGATTCTCCTGACG  
 1 MetArgThrLeuThrIleAsnThrAspAlaGluGlyPheValLeuArgIleLeuLeuThr 20  
 AACGACGATGGAATCTACTCCAACGGACTGCGCGCCGCTGTGAAAGCCCTGAGTGAGCTC  
 21 AsnAspAspGlyIleTyrSerAsnGlyLeuArgAlaAlaValLysAlaLeuSerGluLeu 40  
 GGCGAAGTTTACGTCGTTGCCCCCTCTTCCAGAGGAGCGCGAGCGGCAGGGCCATGACG  
 41 GlyGluValTyrValValAlaProLeuPheGlnArgSerAlaSerGlyArgAlaMetThr 60  
 CTCCACAGGCCGATAAGGGCCAAGCGCGTTGACGTTCCCGGCGCAAAGATAGCCTACGGA  
 61 LeuHisArgProIleArgAlaLysArgValAspValProGlyAlaLysIleAlaTyrGly 80  
 ATAGATGGAACCTCCTACTGACTGCGTGATTTTCGCCATAGCCCGCTTCGGGAGCTTTGGT  
 81 IleAspGlyThrProThrAspCysValIlePheAlaIleAlaArgPheGlySerPheGly 100  
 TTAGCCGTGAGCGGGATTAACTCGGCGAGAACCTGAGCACCGAGATAACAGTCTCAGGG  
 101 LeuAlaValSerGlyIleAsnLeuGlyGluAsnLeuSerThrGluIleThrValSerGly 120  
 ACGGCCTCCGCTGCCATAGAGGCCCTCAACTCATGGAATTCCGAGCATAGCGATTAGCCTT  
 121 ThrAlaSerAlaAlaIleGluAlaSerThrHisGlyIleProSerIleAlaIleSerLeu 140  
 GAGGTGGAGTGAAGAAGACCCCTCGGCGAGGGTGAGGGGGTTGACTTCTCGGTCTCGACT  
 141 GluValGluTrpLysLysThrLeuGlyGluGlyGluGlyValAspPheSerValSerThr 160  
 CACTTCCTCAAGAGAATCGCGGGAGCCCTCTTGGAGAGAGGTCCTCCTGAGGGCGTTGAC  
 161 HisPheLeuLysArgIleAlaGlyAlaLeuLeuGluArgGlyLeuProGluGlyValAsp 180  
 ATGCTCAACGTCAACGTTCCGAGCGACGCGACGGAGGAAACGGAGATAGCAATCACCCGC  
 181 MetLeuAsnValAsnValProSerAspAlaThrGluGluThrGluIleAlaIleThrArg 200  
 TTAGCCCGGAAGCGCTACTCCCCAACGGTCGAGGAGAGGATTGACCCCAAGGGCAACCCC  
 201 LeuAlaArgLysArgTyrSerProThrValGluGluArgIleAspProLysGlyAsnPro 220  
 TACTACTGGATTGTGCGCAAACCTTGTCCTCAAGACTTCGAGCCAGGGACAGATGCCTACGCC  
 221 TyrTyrTrpIleValGlyLysLeuValGlnAspPheGluProGlyThrAspAlaTyrAla 240  
 CTGAAGGTCGAGAGGAAGGTCAGCGTCACGCCGATAAACATAGATATGACTGCGAGGGTG  
 241 LeuLysValGluArgLysValSerValThrProIleAsnIleAspMetThrAlaArgVal 260  
 GACTTTGAGGAGCTTGTAAGGGTCTGTGGGTGTAA  
 261 AspPheGluGluLeuValArgValLeuTrpValEnd 272



# FIGURE 9A

## *Thermococcus* GU5L5 Phosphatase (26A1A) Complete Gene Sequence (Part 1 of 2)

ATGAAAGGAAAGTCTCTGTGTAGCGGTCTGTTGTTGGGTCTTTAATTTTGAGCCTGATT  
 1 MetLysGlyLysSerLeuValSerGlyLeuLeuLeuGlyLeuLeuIleLeuSerLeuIle 20  
 TCATTCCAGCCAAGCTTTGCATACTCCCCACACGGCGGTGTCAAAAACATCATAATCCTG  
 21 SerPheGlnProSerPheAlaTyrSerProHisGlyGlyValLysAsnIleIleIleLeu 40  
 GTTGGAGACGGCATGGGTCTTGGGCATGTAGAAATTACAAAGCTCGTTTATGGACACTTA  
 41 ValGlyAspGlyMetGlyLeuGlyHisValGluIleThrLysLeuValTyrGlyHisLeu 60  
 AACATGGAAAACCTTCCAGTTACTGGATTTGAGCTTACTGATTCCCTAAGTGGTGAAGTT  
 61 AsnMetGluAsnPheProValThrGlyPheGluLeuThrAspSerLeuSerGlyGluVal 80  
 ACAGATTCTGCTGCGGCAGGAAC TGCAATATCCACTGGAGCTAAAACGTATAATGGTATG  
 81 ThrAspSerAlaAlaAlaGlyThrAlaIleSerThrGlyAlaLysThrTyrAsnGlyMet 100  
 ATTTTCAGTAACCAACATAACCGGAAAGATAGTTAACTTAACAACCCCTACTTGAAGTGGCT  
 101 IleSerValThrAsnIleThrGlyLysIleValAsnLeuThrThrLeuLeuGluValAla 120  
 CAAGAGCTTGGGAAGTCAACAGGGCTGGTCACCACAACAAGGATTACCCATGCAACTCCA  
 121 GlnGluLeuGlyLysSerThrGlyLeuValThrThrThrArgIleThrHisAlaThrPro 140  
 GCAGTTTTTTCGTCCTCCATGTCCCAGATAGGGATATGGAGGGGGAGATACCCAAGCAACTC  
 141 AlaValPheAlaSerHisValProAspArgAspMetGluGlyGluIleProLysGlnLeu 160  
 ATAATGCACAAAGTTAACGTCTTGTGGGTGGTGAAGGGAGAAATTCGATGAGAAAAAT  
 161 IleMetHisLysValAsnValLeuLeuGlyGlyGlyArgGluLysPheAspGluLysAsn 180  
 TTGGAGCTGGCCAAAAAGCAGGGATACAAAGTAGTTTTTCACGAAGGAAGAGCTTGAAAAA  
 181 LeuGluLeuAlaLysLysGlnGlyTyrLysValValPheThrLysGluGluLeuGluLys 200  
 GTTGAAGGAGATTATGTCCTAGGACTCTTTGCAGAAAGTCACATCCCTTACGTATTGGAT  
 201 ValGluGlyAspTyrValLeuGlyLeuPheAlaGluSerHisIleProTyrValLeuAsp 220  
 AGAAAACCCGATGATGTTGGACTTTTAGAAATGGCCAAAAGGCAATTTCAATACTCGAG  
 221 ArgLysProAspAspValGlyLeuLeuGluMetAlaLysLysAlaIleSerIleLeuGlu 240  
 AAGAACCCGAGCGGATTCTTTCTCATGGTTGAGGGCGGAAGGATTGACCATGCAGCCCAT  
 241 LysAsnProSerGlyPhePheLeuMetValGluGlyGlyArgIleAspHisAlaAlaHis 260  
 GGAAACGATGTCGCATCGGTGTTGTCAGAAACTAAGGAGTTTGACGATGTTGTCAGATAC  
 261 GlyAsnAspValAlaSerValValAlaGluThrLysGluPheAspAspValValArgTyr 280  
 GTGCTGGAATATCCGAAGAAGAGGGGAGATACCTTGGTAATAGTGCTTGCCGATCACGAA  
 281 ValLeuGluTyrProLysLysArgGlyAspThrLeuValIleValLeuAlaAspHisGlu 300  
 ACTGGAGGTCTTGCAATAGGTCTAACGTATGGAAATGCAATCGATGAAGATGCCATAAGA  
 301 ThrGlyGlyLeuAlaIleGlyLeuThrTyrGlyAsnAlaIleAspGluAspAlaIleArg 320  
 AAAATAAAAGCAAGCACGTTGAGGATGCCCAAAGAGGTTAAGGCAGGAGTAGTGTA  
 321 LysIleLysAlaSerThrLeuArgMetProLysGluValLysAlaGlySerSerValLys 340

# FIGURE 90

## *Thermococcus* GU5L5 Phosphatase (26A1A) Complete Gene Sequence (Part 2 of 2)

GAGTCCTCAAAGGTATGCCGGATTTGTCCCAACAGAGGAAGAAGTCAGTATATTGAGAAT  
 341 GluSerSerLysValCysArgIleCysProAsnArgGlyArgSerGlnTyrIleGluAsn 360  
 GCGCTGCACTCGACAAACAAGTATGCCCTCTCAAATGCAGTAGCCGATGTTATAAACAGG  
 361 AlaLeuHisSerThrAsnLysTyrAlaLeuSerAsnAlaValAlaAspValIleAsnArg 380  
 CGTATTGGTGTGGATTACCTCCTATGAGCATACAGGAGTTCCAGTTCCGCTCTTAGCT  
 381 ArgIleGlyValGlyPheThrSerTyrGluHisThrGlyValProValProLeuLeuAla 400  
 TACGGTCCCGGGGCAGAGAACTTCAGAGGTTTCTTACACCATGTGGATACAGCAAGATTA  
 401 TyrGlyProGlyAlaGluAsnPheArgGlyPheLeuHisHisValAspThrAlaArgLeu 420  
 GTTGCAAAGTTAATGCTCTTTGGAAGGAGGAATATTCCAGTTACCATTTCAAGCGTGAGC  
 421 ValAlaLysLeuMetLeuPheGlyArgArgAsnIleProValThrIleSerSerValSer 440  
 AGTGTTAAGGGAGACATAACCGGTGATTACAGGGTTGATGAGAAGGATGCCTACGTTACG  
 441 SerValLysGlyAspIleThrGlyAspTyrArgValAspGluLysAspAlaTyrValThr 460  
 CTCATGATGTTTCTCGGAGAAAAAGTGGATAATGAAATTGAAAAGAGAGTCGATATAGAC  
 461 LeuMetMetPheLeuGlyGluLysValAspAsnGluIleGluLysArgValAspIleAsp 480  
 AACACGGCATGGTTGACTTAAATGACGTCATGTTGATTCTCCAGGAAGCTTGA  
 481 AsnAsnGlyMetValAspLeuAsnAspValMetLeuIleLeuGlnGluAlaEnd 498

# FIGURE 10A

## OC9a Phosphatase (27A3A) Complete Gene Sequence (Part 1 of 2)

ATGCCAAGAAATATCGCCGCTGTATGCGCCCTGGCCGCTTTGTTAGGGTCGGCCTGGGCG  
 1 MetProArgAsnIleAlaAlaValCysAlaLeuAlaAlaLeuLeuGlySerAlaTrpAla 20  
 GCCAAAGTTGCCGTCTACCCCTACGACGGAGCCGCTTTGCTGGCGGGGAGCGCTTCGAT  
 21 AlaLysValAlaValTyrProTyrAspGlyAlaAlaLeuLeuAlaGlyGlnArgPheAsp 40  
 TTGCGCATAGAAGCCTCCGAGCTGAAAGGCAATTTAAAGGCTTACCGCATCACCTGGAC  
 41 LeuArgIleGluAlaSerGluLeuLysGlyAsnLeuLysAlaTyrArgIleThrLeuAsp 60  
 GGCCAGCCTCTGGCGGGCCTCGAGCAAACCGCGCAGGGGGCCGGGCAGGCCGAGTGGACC  
 61 GlyGlnProLeuAlaGlyLeuGluGlnThrAlaGlnGlyAlaGlyGlnAlaGluTrpThr 80  
 CTGCGCGGTGCCTTCCTGCGCCCTGGAAGCCACCCCTCGAGGTCAGCCTCACCGACGAC  
 81 LeuArgGlyAlaPheLeuArgProGlySerHisThrLeuGluValSerLeuThrAspAsp 100  
 GCTGGGGAGAGCAGGAAGAGCGTACGTTGGGAGGCTCGGCAGAACCTTCGCTTGCCCCGA  
 101 AlaGlyGluSerArgLysSerValArgTrpGluAlaArgGlnAsnLeuArgLeuProArg 120  
 GCGGCCAAGAATGTGATTCTCTTCATTGGCGACGGGATGGGCTGGAACACCCTCAACGCC  
 121 AlaAlaLysAsnValIleLeuPheIleGlyAspGlyMetGlyTrpAsnThrLeuAsnAla 140  
 GCGCGCATCATCGCCAAAGGCTTTAACCCCGAAAACGGTATGCCCAACGGAAACCTCGAG  
 141 AlaArgIleIleAlaLysGlyPheAsnProGluAsnGlyMetProAsnGlyAsnLeuGlu 160  
 ATCGAGAGTGTTACGTTGGGATGGCTACCGTCACTACCGGCAGCTTTGATAGCTTCATC  
 161 IleGluSerGlyTyrGlyGlyMetAlaThrValThrThrGlySerPheAspSerPheIle 180  
 GCGGACTCAGCTAACTCGGCTTCTTCCATCATGACCGGGCAGAAGGTGCAGGTGAATGCC  
 181 AlaAspSerAlaAsnSerAlaSerSerIleMetThrGlyGlnLysValGlnValAsnAla 200  
 CTCAACGTTTACCCATCAAACCTCAAAGATACCTGGCCTACCCCGGATCGAAACCTTA  
 201 LeuAsnValTyrProSerAsnLeuLysAspThrLeuAlaTyrProArgIleGluThrLeu 220  
 GCGGAGATGCTCAAGCGGGTACGCGGGGCCAGCATTGGGGTAGTGACCACCACCTTCGGC  
 221 AlaGluMetLeuLysArgValArgGlyAlaSerIleGlyValValThrThrThrPheGly 240  
 ACCGACGCTACCCCGGCTTCACTCAACGCCCATAACCGCCGCCGCGGTGATTACCAGGCT  
 241 ThrAspAlaThrProAlaSerLeuAsnAlaHisThrArgArgArgGlyAspTyrGlnAla 260  
 ATCGCCGACATGTACTTTGGTAGAGGCGGGTTCGGTGTTCCTTGGATGTGATGCTCTTC  
 261 IleAlaAspMetTyrPheGlyArgGlyGlyPheGlyValProLeuAspValMetLeuPhe 280  
 GGTGGTTACGCGACTTCATCCCCAGAGCACCCCTGGCTCGCGGCGCAAGGATAGCACG  
 281 GlyGlySerArgAspPheIleProGlnSerThrProGlySerArgArgLysAspSerThr 300  
 GACTGGATTGCCGAATCCCAGAAGCTGGGCTACACCTTTGTCAGCACCCGAGCGAGCTG  
 301 AspTrpIleAlaGluSerGlnLysLeuGlyTyrThrPheValSerThrArgSerGluLeu 320  
 CTGGCGGCCAAACCCACCGATAAGCTGTTTGGGCTGTTCAACATTGACAACTTCCCCAGC  
 321 LeuAlaAlaLysProThrAspLysLeuPheGlyLeuPheAsnIleAspAsnPheProSer 340

[illegible]

## OC9a Phosphatase (27A3A)

	TACCTAGACCGCCAGTGTGGAAAGCGGCCGAGATGCTGGGAAGCTTTACCGATATGCCC	
341	TyrLeuAspArgAlaValTrpLysArgProGluMetLeuGlySerPheThrAspMetPro	360
	TACCTCTGGGAGATGACCCAGAAAGCCGTGGAGGCTCTCTCCAGAAACGACAAAGGCTTT	
361	TyrLeuTrpGluMetThrGlnLysAlaValGluAlaLeuSerArgAsnAspLysGlyPhe	380
	TTCTTGATGGTTGAGGGGGGAATGGTGGATAAGTACGAGCACCCTTGGACTGGCCCCGC	
381	PheLeuMetValGluGlyGlyMetValAspLysTyrGluHisProLeuAspTrpProArg	400
	GCACTTTGGGATGTACTCGAGCTGGACCGCGCGGTGGCTTGGGCCAAGGGCTATGCGGCC	
401	AlaLeuTrpAspValLeuGluLeuAspArgAlaValAlaTrpAlaLysGlyTyrAlaAla	420
	TCCCACCCCGATACCCTGGTGATTGTCACCGCCGACCACGCTCACTCGATCTCGGTGTTT	
421	SerHisProAspThrLeuValIleValThrAlaAspHisAlaHisSerIleSerValPhe	440
	GGCGGTTACGACTACTCCAAGCAGGGCCGGGAGGGGGTGGGGGTTATGAGGCCGCCAAG	
441	GlyGlyTyrAspTyrSerLysGlnGlyArgGluGlyValGlyValTyrGluAlaAlaLys	460
	TTCCCCACCTACGGCGACAAAAAAGACGCCAACGGCTTTCCCTTGCCCCGACCACTCGG	
461	PheProThrTyrGlyAspLysLysAspAlaAsnGlyPheProLeuProAspThrThrArg	480
	GGAATCGCGGTAGGCTTCGGGGCCACGCCGATTACTGTGAAACCTACCGGGGCCCGAG	
481	GlyIleAlaValGlyPheGlyAlaThrProAspTyrCysGluThrTyrArgGlyArgGlu	500
	GTCTACAAAGACCCACCATCTCCGACGGCAAAGGTGGTTACGTGGCCAACCTGAGGTC	
501	ValTyrLysAspProThrIleSerAspGlyLysGlyGlyTyrValAlaAsnProGluVal	520
	TGCAAGGAGCCGGGCCTTCCAACGTAACCGGCAACTCCAGTAGATAGCGCCAGGGCGTG	
521	CysLysGluProGlyLeuProThrTyrArgGlnLeuProValAspSerAlaGlnGlyVal	540
	CACACGGCTGATCCCATGCCGCTGTTTGCCCTTGGCGTGGGTCTCAGTTCTTCAATGGC	
541	HisThrAlaAspProMetProLeuPheAlaPheGlyValGlySerGlnPhePheAsnGly	560
	CTCATCGACCAGACCGAGATCTTCTTCCGCATGGCCCAGGCCCTAGGGTTCAACCCCCAC	
561	LeuIleAspGlnThrGluIlePhePheArgMetAlaGlnAlaLeuGlyPheAsnProHis	580
	CTCGAGAAGCCTTAA	
581	LeuGluLysProEnd	585

	AY	BY	CY	DY	EY	FY	GY	HY	IY	JY	KY	LY	MY	NY	OY	PY	QY	R	S	T	U	V	W	X	Y	Z	aa	ab	ac	ad	ae	af	ag	ah	ai	aj	ak	al	am	an	ao	ap	aq	ar	as	at	au	av	aw	ax	ay	az	ba	bb	bc	bd	be	bf	bg	bh	bi	bj	bk	bl	bm	bn	bo	bp	bq	br	bs	bt	bu	bv	bw	bx	by	bz	ca	cb	cc	cd	ce	cf	cg	ch	ci	cj	ck	cl	cm	cn	co	cp	cq	cr	cs	ct	cu	cv	cw	cx	cy	cz	da	db	dc	dd	de	df	dg	dh	di	dj	dk	dl	dm	dn	do	dp	dq	dr	ds	dt	du	dv	dw	dx	dy	dz	ea	eb	ec	ed	ee	ef	eg	eh	ei	ej	ek	el	em	en	eo	ep	eq	er	es	et	eu	ev	ew	ex	ey	ez	fa	fb	fc	fd	fe	ff	fg	fh	fi	fj	fk	fl	fm	fn	fo	fp	fq	fr	fs	ft	fu	fv	fw	fx	fy	fz	ga	gb	gc	gd	ge	gf	gg	gh	gi	gj	gk	gl	gm	gn	go	gp	gq	gr	gs	gt	gu	gv	gw	gx	gy	gz	ha	hb	hc	hd	he	hf	hg	hh	hi	hj	hk	hl	hm	hn	ho	hp	hq	hr	hs	ht	hu	hv	hw	hx	hy	hz	ia	ib	ic	id	ie	if	ig	ih	ii	ij	ik	il	im	in	io	ip	iq	ir	is	it	iu	iv	iw	ix	iy	iz	ja	jb	jc	jd	je	jf	jj	jh	ji	jj	jk	jl	jm	jn	jo	jp	jq	jr	js	jt	ju	jv	jw	jx	ky	kz	la	lb	lc	ld	le	lf	lg	lh	li	lj	lk	ll	lm	ln	lo	lp	lq	lr	ls	lt	lu	lv	lw	lx	ly	lz	ma	mb	mc	md	me	mf	mg	mh	mi	mj	mk	ml	mm	mn	mo	mp	mq	mr	ms	mt	mu	mv	mw	mx	my	mz	na	nb	nc	nd	ne	nf	ng	nh	ni	nj	nk	nl	nm	nn	no	np	nq	nr	ns	nt	nu	nv	nw	nx	ny	nz	oa	ob	oc	od	oe	of	og	oh	oi	oj	ok	ol	om	on	oo	op	oq	or	os	ot	ou	ov	ow	ox	oy	oz	pa	pb	pc	pd	pe	pf	pg	ph	pi	pj	pk	pl	pm	pn	po	pp	pq	pr	ps	pt	pu	pv	pw	px	py	pz	qa	qb	qc	qd	qe	qf	qg	qh	qi	qj	qk	ql	qm	qn	qo	qp	qq	qr	qs	qt	qu	qv	qw	qx	qy	qz	ra	rb	rc	rd	re	rf	rg	rh	ri	rj	rk	rl	rm	rn	ro	rp	rq	rr	rs	rt	ru	rv	rw	rx	ry	rz	sa	sb	sc	sd	se	sf	sg	sh	si	sj	sk	sl	sm	sn	so	sp	sq	sr	ss	st	su	sv	sw	sx	sy	sz	ta	tb	tc	td	te	tf	tg	th	ti	tj	tk	tl	tm	tn	to	tp	tq	tr	ts	tt	tu	tv	tw	tx	ty	tz	ua	ub	uc	ud	ue	uf	ug	uh	ui	uj	uk	ul	um	un	uo	up	uq	ur	us	ut	uu	uv	uw	ux	uy	uz	va	vb	vc	vd	ve	vf	vg	vh	vi	vj	vk	vl	vm	vn	vo	vp	vq	vr	vs	vt	vu	vv	vw	vx	vy	vz	wa	wb	wc	wd	we	wf	wg	wh	wi	wj	wk	wl	wm	wn	wo	wp	wq	wr	ws	wt	wu	wv	ww	wx	wy	wz	xa	xb	xc	xd	xe	xf	xg	xh	xi	xj	xk	xl	xm	xn	xo	xp	xq	xr	xs	xt	xu	xv	xw	xx	xy	xz	ya	yb	yc	yd	ye	yf	yg	yh	yi	yj	yk	yl	ym	yn	yo	yp	yq	yr	ys	yt	yu	yv	yw	yx	yy	yz	za	zb	zc	zd	ze	zf	zg	zh	zi	zj	zk	zl	zm	zn	zo	zp	zq	zr	zs	zt	zu	zv	zw	zx	zy	zz	AA	AB	
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	ATGTATAAATGGATTATTGAGGGTAAGCTTGCCCCAAGCACCTTTTCCAAGCCTAGGTGAA	
1	MetTyrLysTrpIleIleGluGlyLysLeuAlaGlnAlaProPheProSerLeuGlyGlu	20
	CTAGCCGATCTCAAAAGACTTTTCGACGCCATTATTGTTCTTACAATGCCGCATGAACAA	
21	LeuAlaAspLeuLysArgLeuPheAspAlaIleIleValLeuThrMetProHisGluGln	40
	CCGCTTAATGAGAAATATATCGAGATATTAGAGAGCCATGGATTCCAAGTCCTCCATGTC	
41	ProLeuAsnGluLysTyrIleGluIleLeuGluSerHisGlyPheGlnValLeuHisVal	60
	CCCACGCTCGACTTTTCATCCTTTTGAAGCTCTTCGACCTTTTGAAAACAAGCATATTCATT	
61	ProThrLeuAspPheHisProLeuGluLeuPheAspLeuLeuLysThrSerIlePheIle	80
	GATGAAAACCTGGAGAGATCCACAGAGTGCTTGTCCTGTCATGGGAGGCATAGGCCGG	
81	AspGluAsnLeuGluArgSerHisArgValLeuValHisCysMetGlyGlyIleGlyArg	100
	AGCGGGCTTGTAAGTGTGCGTACTTAATATTCAAAGGTTATGATATTTACGACGCGGTA	
101	SerGlyLeuValThrAlaAlaTyrLeuIlePheLysGlyTyrAspIleTyrAspAlaVal	120
	AAGCATGTGAGAACGGTAGTGCCTGGTGCTATTGAAAACAGAGGGCAAGCGTTAATGCTT	
121	LysHisValArgThrValValProGlyAlaIleGluAsnArgGlyGlnAlaLeuMetLeu	140
	GAGAACTACTATACCCTGGTCAAAAGTTTCAACAGAGAGTTGCTGAGAGACTACGGGAAG	
141	GluAsnTyrTyrThrLeuValLysSerPheAsnArgGluLeuLeuArgAspTyrGlyLys	160
	AAAATTTTCACGCTCGGTGACCCGAAGGCGGTTCTCCACGCTTCTAAGACGACTCAGTTC	
161	LysIlePheThrLeuGlyAspProLysAlaValLeuHisAlaSerLysThrThrGlnPhe	180
	ACGATTGAACTCTTAAGCAACTTACACGTCAACGAGGCGTTTTCAATCAGTGCGATGGCT	
181	ThrIleGluLeuLeuSerAsnLeuHisValAsnGluAlaPheSerIleSerAlaMetAla	200
	CAATCACTGCTCCACTTTCACGACGTAAAGTCCGCTCTAAACTGAAAGAAGTATTCGAA	
201	GlnSerLeuLeuHisPheHisAspValLysValArgSerLysLeuLysGluValPheGlu	220
	AACATGGAATTCTCATCCGCCTCAGAGGAGGTTCTGTCATTTATTCACCTACTCGATTTT	
221	AsnMetGluPheSerSerAlaSerGluGluValLeuSerPheIleHisLeuLeuAspPhe	240
	TATCAGGATGGCAGGGTTGTTTTAACCATTTACGATTATCTCCCCGATAGGGTGGATTTG	
241	TyrGlnAspGlyArgValValLeuThrIleTyrAspTyrLeuProAspArgValAspLeu	260
	ATTTTATTGTGTAAGTGGGGTTGTGATAAAATAGTTGAAGTCTCGTCTTCAGCGAAGAAA	
261	IleLeuLeuCysLysTrpGlyCysAspLysIleValGluValSerSerSerAlaLysLys	280
	ACCGTTGAGAAGCTTGTAGGAAGAAAGGTTTCCCTATCTCGGGCTAATTACTTAGACTAT	
281	ThrValGluLysLeuValGlyArgLysValSerLeuSerTrpAlaAsnTyrLeuAspTyr	300
	GTTTAC	
301	ValEnd	302

# FIGURE 12

## *Thermococcus* CL-2 Phosphatase (30A1A) Complete Gene Sequence

ATGAGAATCCTCCTCACCAACGACGACGGCATCTATTCCAACGGTCTGCGCGCGGCGGTG  
 1 MetArgIleLeuLeuThrAsnAspAspGlyIleTyrSerAsnGlyLeuArgAlaAlaVal 20  
 AAGGGCCTGAGCGAGCTCGGCGAGGTCTACGTCGTCGCCCCGCTCTTCCAGAGGAGCGCG  
 21 LysGlyLeuSerGluLeuGlyGluValTyrValValAlaProLeuPheGlnArgSerAla 40  
 AGCGGTCGGGCGATGACCCTACACAGGCCGATAAGGGCAAAGAGGGTTGACGTTCCCGGC  
 41 SerGlyArgAlaMetThrLeuHisArgProIleArgAlaLysArgValAspValProGly 60  
 GCGAAGATAGCGTATGGCATAGACGGAACGCCGACCGACTGCGTGATTTTTGCCATCGCC  
 61 AlaLysIleAlaTyrGlyIleAspGlyThrProThrAspCysValIlePheAlaIleAla 80  
 CGCTTCGGCGACTTTGATCTGGCGGTCTAGCGGGATAAACCTAGGCGAGAACCTGAGCACG  
 81 ArgPheGlyAspPheAspLeuAlaValSerGlyIleAsnLeuGlyGluAsnLeuSerThr 100  
 GAGATAACCGTCTCCGGAACGGCCTCGGCGGCGATAGAGGCTTCCACCCACGGGATTCCA  
 101 GluIleThrValSerGlyThrAlaSerAlaAlaIleGluAlaSerThrHisGlyIlePro 120  
 AGTGTAGCTATAAGCCTCGAGGTCGAGTGAAGAAGACCCTCGGCGAGGGGGAGGGTATT  
 121 SerValAlaIleSerLeuGluValGluTrpLysLysThrLeuGlyGluGlyGluGlyIle 140  
 GACTTCTCGGTTTCAGCACACTTCCTGAGAAGGATAGCGACGGCTGTCCTTAAGAAGGGC  
 141 AspPheSerValSerAlaHisPheLeuArgArgIleAlaThrAlaValLeuLysLysGly 160  
 CTGCCTGAAGGGGTGGACATGCTCAACGTGAACGTCCCTAGCGACGCCAGCGAGGGGACT  
 161 LeuProGluGlyValAspMetLeuAsnValAsnValProSerAspAlaSerGluGlyThr 180  
 GAGATCGCCATAACGCGCCTCGCGAGGAAGCGCTATTCTCCGACGATAGAGGAGAGGATA  
 181 GluIleAlaIleThrArgLeuAlaArgLysArgTyrSerProThrIleGluGluArgIle 200  
 GACCCCAAGGGCAACCCCTACTACTGGATCGTTGGCAGGCTCGTCCAGGAGTTCGAGCCG  
 201 AspProLysGlyAsnProTyrTyrTrpIleValGlyArgLeuValGlnGluPheGluPro 220  
 GGCACGGACGCCTACGCTCTGAAAGTCGAGAGAAAGGTCAGCGTCACGCCCATAAACATC  
 221 GlyThrAspAlaTyrAlaLeuLysValGluArgLysValSerValThrProIleAsnIle 240  
 GACATGACTGCGAGGGTTGACTTTGAGAACCTTCAAAGGCTTCTGAGCCTGTGA  
 241 AspMetThrAlaArgValAspPheGluAsnLeuGlnArgLeuLeuSerLeuEnd 258

**Aquifex VF-5 Phosphatase (34A1A)**  
**Complete Gene Sequence**

1	ATGGAAACTTAAAAAAGTACCTAGAAAGTTGCAAAAATAGCCGCGCTCGCGGGTGGGCAG MetGluAsnLeuLysLysTyrLeuGluValAlaLysIleAlaAlaLeuAlaGlyGlyGln	20
21	GTTCTGAAAGAAACTTCGGAAAGGTAAAAAAGGAAAACATAGAGGAAAAAGGGGAAAAG ValLeuLysGluAsnPheGlyLysValLysLysGluAsnIleGluGluLysGlyGluLys	40
41	GACTTTGTAAAGTTACGTGGATAAAACTTCAGAGGAAAGGATAAAGGAGGTGATACTCAAG AspPheValSerTyrValAspLysThrSerGluGluArgIleLysGluValIleLeuLys	60
61	TTCTTTCCCGATCACGAGGTCGTAGGGGAAGAGATGGGTGCGGAGGGAAGCGGAAGCGAA PhePheProAspHisGluValValGlyGluGluMetGlyAlaGluGlySerGlySerGlu	80
81	TACAGGTGGTTTCATAGACCCCTTGACGGCACAAAGAACTACATAAACGGTTTTCCCATC TyrArgTrpPheIleAspProLeuAspGlyThrLysAsnTyrIleAsnGlyPheProIle	100
101	TTTGCCGTATCAGTGGGACTTGTTAAGGGAGAAGAGCCAATTGTGGGTGCGGTTTACCTT PheAlaValSerValGlyLeuValLysGlyGluGluProIleValGlyAlaValTyrLeu	120
121	CCTTACTTTGACAAGCTTTACTGGGGTGCTAAAGGTCTCGGGGCTTACGTAAACGGAAAG ProTyrPheAspLysLeuTyrTrpGlyAlaLysGlyLeuGlyAlaTyrValAsnGlyLys	140
141	AGGATAAAGGTAAAGGACAATGAGAGTTTAAAGCACGCCGGAGTGGTTTACGGATTTCCC ArgIleLysValLysAspAsnGluSerLeuLysHisAlaGlyValValTyrGlyPhePro	160
161	TCTAGGAGCAGGAGGGACATATCTATCTACTTGAACATATTCAAGGATGTCTTTTACGAA SerArgSerArgArgAspIleSerIleTyrLeuAsnIlePheLysAspValPheTyrGlu	180
181	GTTGGCTCTATGAGGAGACCCGGGGCTGCTGCGGTTGACCTCTGCATGGTGGCGGAAGGG ValGlySerMetArgArgProGlyAlaAlaAlaValAspLeuCysMetValAlaGluGly	200
201	ATATTTGACGGGATGATGGAGTTTGAATGAAGCCGTGGGACATAACCGCAGGGCTTGTA IlePheAspGlyMetMetGluPheGluMetLysProTrpAspIleThrAlaGlyLeuVal	220
221	ATACTGAAGGAAGCCGGGGGCGTTTACACACTTGTGGGAGAACCCTTCGGAGTTTCGGAC IleLeuLysGluAlaGlyGlyValTyrThrLeuValGlyGluProPheGlyValSerAsp	240
241	ATAATTGCGGGCAACAAAGCCCTCCACGACTTTTATACTTCAGGTAGCCAAAAGTATATG IleIleAlaGlyAsnLysAlaLeuHisAspPheIleLeuGlnValAlaLysLysTyrMet	260
261	GAAGTGGCGGTGTGA GluValAlaValEnd	265